

WEST Search History

10/797,366

[Hide Items Restore Clear Cancel]

DATE: Tuesday, December 19, 2006

Hide? Set Name Query Hit Count*DB=USPT; PLUR=YES; OP=ADJ*

<input type="checkbox"/>	L16	6965015	1
<input type="checkbox"/>	L15	6965011	1
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<input type="checkbox"/>	L8	6818449	1
<input type="checkbox"/>	L7	6806352	2
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<input type="checkbox"/>	L5	6723535	1
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<input type="checkbox"/>	L2	6635468	1
<input type="checkbox"/>	L1	09907794	0

END OF SEARCH HISTORY

<!--StartFragment-->

ALIGNMENTS

RESULT 1

A59180

Wnt inhibitory factor-1 - human

C;Species: Homo sapiens (man)

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004

C;Accession: A59180

R;Hsieh, J.C.; Kodjabachian, L.; Rebbert, M.L.; Rattner, A.; Smallwood, P.M.; Samos, C
Nature 398, 431-436, 1999A;Title: A new secreted protein that binds to Wnt proteins and inhibits their activiti
A;Reference number: A59180; MUID:99215557; PMID:10201374

A;Accession: A59180

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-379 <HSI>

A;Cross-references: UNIPROT:Q9Y5W5; UNIPARC:UPI0000051058; GB:AF122922; NID:g4585369;

Query Match 99.7%; Score 2142; DB 2; Length 379;
 Best Local Similarity 99.7%; Pred. No. 1.2e-142;
 Matches 378; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSE 60

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSE 60

Qy 61 GKMAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEFYEFSLRSLDKGIMADPTVN 120

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 GKMAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEFYEFSLRSLDKGIMADPTVN 120

Qy 121 VPLLGTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQA 180

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 VPLLGTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQA 180

Qy 181 ECPGGCRNGGFNCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVN 240

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 ECPGGCRNGGFNCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVN 240

Qy 241 CDKANCSTTCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGY 300

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 CDKANCSTTCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGY 300

Qy 301 QGDLC SKPVCE PGCGA HGT CHEPN KCQC QEG WHGR HCN KRYE ASLI HALR PAGA QLRQHT 360

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 QGDLC SKPVCE PGCGA HGT CHEPN KCQC QEG WHGR HCN KRYE ASLI HALR PAGA QLRQHT 360

Qy 361 PSLKKAERRDPPE SNYIW 379

||| ||| ||| ||| |||

Db 361 PSLKKAERRDPPE SNYIW 379

<!--EndFragment-->

<!--StartFragment-->RESULT 1

WIF1_HUMAN

ID WIF1_HUMAN STANDARD; PRT; 379 AA.

AC Q9Y5W5; Q6UXI1; Q8WVG4;

DT 11-JAN-2001, integrated into UniProtKB/Swiss-Prot.

DT 15-MAR-2005, sequence version 3.

DT 07-MAR-2006, entry version 45.

DE Wnt inhibitory factor 1 precursor (WIF-1).

GN Name=WIF1; ORFNames=UNQ191/PRO217;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA].

RX MEDLINE=99215557; PubMed=10201374; DOI=10.1038/18899;

RA Hsieh J.-C., Kodjabachian L., Rebbert M.L., Rattner A.,

RA Smallwood P.M., Samos C.H., Nusse R., Dawid I.B., Nathans J.;

RT "A new secreted protein that binds to Wnt proteins and inhibits their activities.";

RL Nature 398:431-436 (1999).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].

RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

RA Wood W.I., Godowski P.J., Gray A.M.;

RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";

RL Genome Res. 13:2265-2270 (2003).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].

RC TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!!- FUNCTION: Binds to WNT proteins and inhibits their activities. May
 CC be involved in mesoderm segmentation.
 CC -!!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!!- SIMILARITY: Contains 5 EGF-like domains.
 CC -!!- SIMILARITY: Contains 1 WIF domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AF122922; AAD25402.1; -; mRNA.
 DR EMBL; AY358344; AAQ88710.1; -; mRNA.
 DR EMBL; BC018037; AAH18037.1; -; mRNA.
 DR PIR; A59180; A59180.
 DR HSSP; P05107; 1L3Y.
 DR Ensembl; ENSG00000156076; Homo sapiens.
 DR HGNC; HGNC:18081; WIF1.
 DR MIM; 605186; gene.
 DR GO; GO:0007165; P:signal transduction; NAS.
 DR InterPro; IPR006210; EGF.
 DR InterPro; IPR000742; EGF_3.
 DR InterPro; IPR013111; EGF_extracell.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR013032; EGF_like_reg.
 DR InterPro; IPR003306; WIF.
 DR InterPro; IPR013309; WIF1.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF07974; EGF_2; 3.
 DR Pfam; PF02019; WIF; 1.
 DR PRINTS; PR01901; WIFPROTEIN.
 DR SMART; SM00181; EGF; 5.
 DR SMART; SM00469; WIF; 1.
 DR PROSITE; PS00022; EGF_1; 5.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS50026; EGF_3; 5.
 DR PROSITE; PS50814; WIF; 1.
 KW Developmental protein; EGF-like domain; Glycoprotein; Repeat; Signal;
 KW Wnt signaling pathway.
 FT SIGNAL 1 28 Potential.
 FT CHAIN 29 379 Wnt inhibitory factor 1.
 FT /FTId=PRO_0000007775.
 FT DOMAIN 38 176 WIF.
 FT DOMAIN 177 208 EGF-like 1.
 FT DOMAIN 209 240 EGF-like 2.
 FT DOMAIN 241 272 EGF-like 3.
 FT DOMAIN 273 304 EGF-like 4.
 FT DOMAIN 305 336 EGF-like 5.
 FT CARBOHYD 88 88 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 245 245 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 177 186 Potential.
 FT DISULFID 182 192 Potential.
 FT DISULFID 198 200 Potential.
 FT DISULFID 209 218 Potential.
 FT DISULFID 214 224 Potential.
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 FT DISULFID 241 250 Potential.
 FT DISULFID 246 256 Potential.
 FT DISULFID 262 264 Potential.
 FT DISULFID 273 282 Potential.
 FT DISULFID 278 288 Potential.
 FT DISULFID 294 296 Potential.

FT DISULFID 305 314 Potential.
 FT DISULFID 310 320 Potential.
 FT DISULFID 326 328 Potential.
 FT CONFLICT 166 166 Q -> K (in Ref. 3).
 FT CONFLICT 178 178 Q -> L (in Ref. 1).
 SQ SEQUENCE 379 AA; 41528 MW; 32ADFA6644833E9D CRC64;

Query Match 100.0%; Score 2149; DB 1; Length 379;
 Best Local Similarity 100.0%; Pred. No. 3.9e-158;
 Matches 379; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSE 60
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 Db 1 MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSE 60
 Qy 61 GKMAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVN 120
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 Db 61 GKMAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVN 120
 Qy 121 VPLLGTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQA 180
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 Db 121 VPLLGTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQA 180
 Qy 181 ECPGGCRNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVN 240
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 Db 181 ECPGGCRNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVN 240
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 Db 241 CDKANCSTTCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGY 300
 Qy 301 QGDLCSPKVCEPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHT 360
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 Db 301 QGDLCSPKVCEPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHT 360
 Qy 361 PSLKKAERRDPPESNYIW 379
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 Db 361 PSLKKAERRDPPESNYIW 379
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